NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☒ 7. Other: _See attached error report._

Applicant Must Provide:

☒ An initial or <u>substitute</u> computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or <u>substitute</u> paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
Patentln Software Program Support
    Technical Assistance...................................703-287-0200
    To Purchase PatentIn Software........................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: 09/591,632 C

Source: 1Full

Date Processed by STIC: 2/7/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
   http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	**SUGGESTED CORRECTION**	SERIAL NUMBER: _09/591,632C_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
       Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                          prevent "wrapping."

2____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
       Numbering   use space characters, instead.

4____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                          ensure your subsequent submission is saved in ASCII text.

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                          each n or Xaa can only represent a single residue. Please present the maximum number of each
                          residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
       "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                          previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                          the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                          Artificial or Unknown sequences.

7____Skipped Sequences   Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence:
       (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                          (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                          (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                          This sequence is intentionally skipped

                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences   Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence.
       (NEW RULES)   <210> sequence id number
                          <400> sequence id number
                          000

9____Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
       (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                          In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
       Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                          is Artificial Sequence

11____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                          Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                          "Unknown." Please explain source of genetic material in <220> to <223> section.
                          (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
       "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                          listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/591,632C

DATE: 02/07/2006
TIME: 09:01:23

Input Set : A:\34978a.txt
Output Set: N:\CRF4\02072006\I591632C.raw

[handwritten: list exceeds 72 characters]

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  3  <110> APPLICANT: Lindquist, et al.
  5  <120> TITLE OF INVENTION: RECOMBINANT PRION-LIKE GENES AND PROTEINS AND MATERIALS AND
  6        METHODS COMPRISING SAME
  8  <130> FILE REFERENCE: 30554/34978A
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/591,632C
C--> 10 <141> CURRENT FILING DATE: 2000-06-09
    10 <150> PRIOR APPLICATION NUMBER: US 09/591,632
    11 <151> PRIOR FILING DATE: 2000-06-09
    13 <150> PRIOR APPLICATION NUMBER: US 60/138,833
    14 <151> PRIOR FILING DATE: 1999-06-09
    16 <160> NUMBER OF SEQ ID NOS: 70
    18 <170> SOFTWARE: PatentIn version 3.3
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[handwritten annotations: "(see item 2 on Error summary sheet)", "delete – these are not prior data. They are current data.", "Does Not Comply / Corrected Diskette Needed", "pp 1,3,5-6,7"]

ERRORED SEQUENCES

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   430 <211> LENGTH: 1427
   431 <212> TYPE: DNA
   432 <213> ORGANISM: Saccharomyces cerevisiae
   434 <220> FEATURE:
   435 <221> NAME/KEY: CDS
   436 <222> LOCATION: (182)..(1246)
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   443 agtttttcat tttttgttat tagtcatatt gttttaagct gcaaattaag ttgtacacca     180
   445 a atg atg aat aac aac ggc aac caa gtg tcg aat ctc tcc aat gcg ctc      229
   446   Met Met Asn Asn Asn Gly Asn Gln Val Ser Asn Leu Ser Asn Ala Leu
   447   1               5                   10                  15
   449 cgt caa gta aac ata gga aac agg aac agt aat aca acc acc gat caa        277
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   451             20                  25                  30
   453 agt aat ata aat ttt gaa ttt tca aca ggt gta aat aat aat aat aat       325
   454 Ser Asn Ile Asn Phe Glu Phe Ser Thr Gly Val Asn Asn Asn Asn Asn
   455         35                  40                  45
   457 aac aat agc agt agt aat aac aat aat gtt caa aac aat aac agc ggc       373
   458 Asn Asn Ser Ser Ser Asn Asn Asn Asn Val Gln Asn Asn Asn Ser Gly
   459     50                  55                  60
   461 cgc aat ggt agc caa aat aat gat aac gag aat aat atc aag aat acc       421
   462 Arg Asn Gly Ser Gln Asn Asn Asp Asn Glu Asn Asn Ile Lys Asn Thr
   463 65                  70                  75                  80
   465 tta gaa caa cat cga caa caa caa cag gca ttt tcg gat atg agt cac       469
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RAW SEQUENCE LISTING   DATE: 02/07/2006
PATENT APPLICATION: US/09/591,632C   TIME: 09:01:23

Input Set : A:\34978a.txt
Output Set: N:\CRF4\02072006\I591632C.raw

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470 Val Glu Tyr Ser Arg Ile Thr Lys Phe Phe Gln Glu Gln Pro Leu Glu
471              100             105             110
473 gga tat acc ctt ttc tct cac agg tct gcg cct aat gga ttc aaa gtt    565
474 Gly Tyr Thr Leu Phe Ser His Arg Ser Ala Pro Asn Gly Phe Lys Val
475              115             120             125
477 gct ata gta cta agt gaa ctt gga ttt cat tat aac aca atc ttc cta    613
478 Ala Ile Val Leu Ser Glu Leu Gly Phe His Tyr Asn Thr Ile Phe Leu
479              130             135             140
481 gat ttc aat ctt ggc gaa cat agg gcc ccc gaa ttt gtg tct gtg aac    661
482 Asp Phe Asn Leu Gly Glu His Arg Ala Pro Glu Phe Val Ser Val Asn
483 145             150             155             160
485 cct aat gca aga gtt cca gct tta atc gat cat ggt atg gac aac ttg    709
486 Pro Asn Ala Arg Val Pro Ala Leu Ile Asp His Gly Met Asp Asn Leu
487              165             170             175
489 tct att tgg gaa tca ggg gcg att tta tta cat ttg gta aat aaa tat    757
490 Ser Ile Trp Glu Ser Gly Ala Ile Leu Leu His Leu Val Asn Lys Tyr
491              180             185             190
493 tac aaa gag act ggt aat cca tta ctc tgg tcc gat gat tta gct gac    805
494 Tyr Lys Glu Thr Gly Asn Pro Leu Leu Trp Ser Asp Asp Leu Ala Asp
495              195             200             205
497 caa tca caa atc aac gca tgg ttg ttc ttc caa acg tca ggg cat gcg    853
498 Gln Ser Gln Ile Asn Ala Trp Leu Phe Phe Gln Thr Ser Gly His Ala
499 210             215             220
501 cca atg att gga caa gct tta cat ttc aga tac ttc cat tca caa aag    901
502 Pro Met Ile Gly Gln Ala Leu His Phe Arg Tyr Phe His Ser Gln Lys
503 225             230             235             240
505 ata gca agt gct gta gaa aga tat acg gat gag gtt aga aga gtt tac    949
506 Ile Ala Ser Ala Val Glu Arg Tyr Thr Asp Glu Val Arg Arg Val Tyr
507              245             250             255
509 ggt gta gtg gag atg gcc ttg gct gaa cgt aga gaa gcg ctg gtg atg    997
510 Gly Val Val Glu Met Ala Leu Ala Glu Arg Arg Glu Ala Leu Val Met
511              260             265             270
513 gaa tta gac acg gaa aat gcg gct gca tac tca gct ggt aca aca cca   1045
514 Glu Leu Asp Thr Glu Asn Ala Ala Ala Tyr Ser Ala Gly Thr Thr Pro
515              275             280             285
517 atg tca caa agt cgt ttc ttt gat tat ccc gta tgg ctt gta gga gat   1093
518 Met Ser Gln Ser Arg Phe Phe Asp Tyr Pro Val Trp Leu Val Gly Asp
519              290             295             300
521 aaa tta act ata gca gat ttg gcc ttt gtc cca tgg aat aat gtc gtg   1141
522 Lys Leu Thr Ile Ala Asp Leu Ala Phe Val Pro Trp Asn Asn Val Val
523 305             310             315             320
525 gat aga att ggc att aat atc aaa att gaa ttt cca gaa gtt tac aaa   1189
526 Asp Arg Ile Gly Ile Asn Ile Lys Ile Glu Phe Pro Glu Val Tyr Lys
527              325             330             335
529 tgg acg aag cat atg atg aga aga ccc gcg gtc atc aag gca ttg cgt   1237
530 Trp Thr Lys His Met Met Arg Arg Pro Ala Val Ile Lys Ala Leu Arg
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     737 acttcaccac cctttatttc aggctgatat cttagccttg ttactagtta gaaaaagaca   180
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     743 ttgtcagaat catataaaag aagaagcaaa taactccttg tcttgtatca attgcattat   360
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          3867 acaacaatct aatgagtacg gaagaccgca atacggcgga aaccagaact ccaatggaca   4440
B--> 3869 gcacgaatcc tttaattttt ctggcaactt ttctcaacag aacaataacg gcaaccagaa   4500 4499
B--> 3871 ccgctacccg cggatggcta gcaaaggaga agaactcttc actggagttg tcccaattct   4560
B--> 3873 tgttgaatta gatggtgatg ttaatgggca caaattttct gtcagtggag agggtgaagg   4620
B--> 3875 tgatgcaaca tacggaaaac ttacccttaa atttatttgc actactggaa aactacctgt   4680
B--> 3877 tccatggcca acacttgtca ctactttcac ttatggtgtt cagtgctttt caagataccc   4740
B--> 3879 ggatcatatg aaacggcatg acttttcaa gagtgccatg cccgaaggtt atgtacagga   4800
B--> 3881 aagaactata tttttcaaag atgacgggaa ctacaagaca cgtgctgaag tcaagtttga   4860
B--> 3883 aggtgatacc cttgttaata gaatcgagtt aaaaggtatt gattttaaag aagatggaaa   4920
B--> 3885 cattcttggg cacaaattgg aatacaacta taactcacac aatgtataca tcatggcaga   4980
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B--> 3893 agaccacatg gtccttcttg agtttgtaac agctgctggg attacacatg gcatggatga   5220
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B--> 3897 tcgttttaca acgtcgtgac tgggaaaacc ctggcgttac ccaacttaat cgccttgcag   5340
B--> 3899 cacatccccc tttcgccagc tggcgtaata gcgaagaggc ccgcaccgat cgcccttccc   5400
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```

RAW SEQUENCE LISTING   DATE: 02/07/2006
PATENT APPLICATION: US/09/591,632C   TIME: 09:01:23

Input Set : A:\34978a.txt
Output Set: N:\CRF4\02072006\I591632C.raw

```
E--> 3959 gggcttgtct gctcccggca tccgcttaca gacaagctgt gaccgtctcc gggagctgca  ⟨7200
E--> 3961 tgtgtcagag gttttcaccg tcatcaccga aacgcgcga                            7239⟩
```

```
gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa tga      720
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp glu Leu Tyr Lys
225             230             235
```

(240) delete, since
no amend
acid
is shown

Input Set : A:\34978a.txt
Output Set: N:\CRF4\02072006\I591632C.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:541 M:254 E: No. of Bases conflict, LENGTH:Input:1427 Counted:1426 SEQ:3
L:541 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1427 Found:1426 SEQ:3
L:747 M:252 E: No. of Seq. differs, <211> LENGTH:Input:446 Found:445 SEQ:11
L:3593 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:39
L:3869 M:254 E: No. of Bases conflict, LENGTH:Input:4500 Counted:4499 SEQ:45
M:254 Repeated in SeqNo=45
L:3961 M:252 E: No. of Seq. differs, <211> LENGTH:Input:7239 Found:7238 SEQ:45